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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/910,208	07/20/2001	Jiro Hitomi	MM4454	4894
1109 7590 02/07/2007 ANDERSON, KILL & OLICK, P.C. 1251 AVENUE OF THE AMERICAS NEW YORK,, NY 10020-1182			EXAMINER HADDAD, MAHER M	
			ART UNIT	PAPER NUMBER
			1644	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	02/07/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.



UNITED STATES DEPARTMENT OF COMMERCE

U.S. Patent and Trademark Office

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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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09/910,208

EXAMINER

Maher Haddad

ART UNIT	PAPER
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1644

20070201

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

The reply filed 12/7/06 to fix the discrepancy between sequence listing and specification in response to the Office Action mailed 3/31/06 and 3/17/05. However, the computer readable form of the the "Sequence Listing" submitted on 12/7/06 is flawed technically. Please see enclosed Raw Sequence Listing Error Report.

Since the above -mention Amendment and response appear to be a bona fide attempt to reply, applicant is given a TIME PERIOD OF (1) MONTH OR THIRTY (30) DAYS, whichever is longer, from the mailing date of this notice within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD UNDER 37 CFR1.136(a) ARE AVAILABLE.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maher Haddad whose telephone number is (571) 272-0845. The examiner can normally be reached Monday through Friday from 9:00 am to 5:30 p.m. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on (571) 272-0841. The IFW official Fax number is (571) 273-8300.

Any information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Maher Haddad

Maher Haddad, 1644

February 1, 2007

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/910,208C
Source: 1FW/6
Date Processed by STIC: 12/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/9/0, 208C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

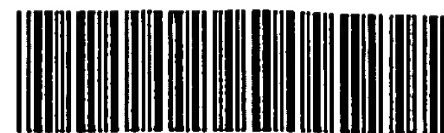
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 12/07/2006

PATENT APPLICATION: US/09/910,208C

TIME: 08:54:18

Input Set : F:\MM4454.ST25.txt

Output Set: N:\CRF4\12072006\I910208C.raw

3 <110> APPLICANT: Hitomi, Jiro
 4 Yamamura, Tokujiro
 5 Kimura, Tatsuji
 6 Yamaguchi, Ken
 8 <120> TITLE OF INVENTION: Novel Calcium-Binding Proteins
 10 <130> FILE REFERENCE: MM4454
 12 <140> CURRENT APPLICATION NUMBER: 09/910,208C
 13 <141> CURRENT FILING DATE: 2001-07-20
 15 <160> NUMBER OF SEQ ID NOS: 20
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 429
 21 <212> TYPE: DNA
 22 <213> ORGANISM: calcium binding protein
 25 <220> FEATURE:
 26 <221> NAME/KEY: exon
 27 <222> LOCATION: (48)..(323)
 28 <223> OTHER INFORMATION: Amino acid sequence of calcium-binding protein from bovine
 29 amniotic fluid
 31 <400> SEQUENCE: 1
 32 ctggcattcc acacttctgt gcagaggggt gaacgtagtt tggtaaa atg act aag 56
 33 Met Thr Lys
 34 1
 36 ctg gaa gat cac ctg gag gga atc atc aac atc ttc cac cag tac tcc 104
 37 Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln Tyr Ser
 38 5 10 15
 40 gtt cgg gtg ggg cat ttc gac acc ctc aac aag cgt gag ctg aag cag 152
 41 Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu Lys Gln
 42 20 25 30 35
 44 ctg atc aca aag gaa ctt ccc aaa acc ctc cag aac acc aaa gat caa 200
 45 Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp Gln
 46 40 45 50
 48 cct acc att gac aaa ata ttc caa gac ctg gat gcc gat aaa gac gga 248
 49 Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys Asp Gly
 50 55 60 65
 52 gcc gtc agc ttt gag gaa ttc gta gtc ctg gtg tcc agg gtg ctg aaa 296
 53 Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val Leu Lys
 54 70 75 80
 56 aca gcc cac ata gat atc cac aaa gag taggaagctc tttccagcaa 343
 57 Thr Ala His Ile Asp Ile His Lys Glu
 58 85 90
 60 tgtccccaag aagacttacc cttctcctcc ctgaggctgc cttacccgag ggaagagaga 403
 62 attaataaac gtactttggc aaagtt 429

see pp 1, 5
 Does Not Comply
 Corrected Diskette Needed

invalid response - see item 10 on Error
 Summary Sheet

If this is an Artificial Sequence
 give sources of genetic material in
 <2207-2223>
 section

RAW SEQUENCE LISTING

DATE: 12/07/2006

PATENT APPLICATION: US/09/910,208C

TIME: 08:54:18

Input Set : F:\MM4454.ST25.txt

Output Set: N:\CRF4\12072006\I910208C.raw

```

65 <210> SEQ ID NO: 2
66 <211> LENGTH: 50
67 <212> TYPE: PRT
68 <213> ORGANISM: Bos taurus
70 <400> SEQUENCE: 2
72 Thr Lys Leu Glu His Leu Glu Gly Ile Ile Asn Ile Phe His Gln Tyr
73 1          5          10          15
76 Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu Lys
77          20          25          30
80 Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp
81          35          40          45
84 Gln Pro
85          50
88 <210> SEQ ID NO: 3
89 <211> LENGTH: 8
90 <212> TYPE: PRT
91 <213> ORGANISM: Bos taurus
93 <400> SEQUENCE: 3
95 Ile Phe Gln Asp Leu Asp Ala Asp
96 1          5
99 <210> SEQ ID NO: 4
100 <211> LENGTH: 12
101 <212> TYPE: PRT
102 <213> ORGANISM: Bos taurus
104 <400> SEQUENCE: 4
106 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu
107 1          5          10
110 <210> SEQ ID NO: 5
111 <211> LENGTH: 9
112 <212> TYPE: PRT
113 <213> ORGANISM: Bos taurus
115 <400> SEQUENCE: 5
117 Thr Ala His Ile Asp Ile His Lys Glu
118 1          5
121 <210> SEQ ID NO: 6
122 <211> LENGTH: 31
123 <212> TYPE: PRT
124 <213> ORGANISM: Bos taurus
126 <400> SEQUENCE: 6
128 Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp Gln Pro Thr Ile Asp Lys
129 1          5          10          15
132 Ile Phe Gln Asp Leu Asp Ala Asp Lys Asp Gly Ala Val Ser Phe
133          20          25          30
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 20
138 <212> TYPE: PRT
139 <213> ORGANISM: Bos taurus
141 <400> SEQUENCE: 7
143 Glu Phe Val Val Leu Val Ser Arg Val Leu Lys Arg Ala His Ile Asp

```

RAW SEQUENCE LISTING

DATE: 12/07/2006

PATENT APPLICATION: US/09/910,208C

TIME: 08:54:18

Input Set : F:\MM4454.ST25.txt

Output Set: N:\CRF4\12072006\I910208C.raw

```

144 1          5          10          15
147 Ile His Lys Glu
148          20
151 <210> SEQ ID NO: 8
152 <211> LENGTH: 20
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial
156 <220> FEATURE:
157 <223> OTHER INFORMATION: sense primer
160 <220> FEATURE:
161 <221> NAME/KEY: misc_feature
162 <222> LOCATION: (3)..(3) /
163 <223> OTHER INFORMATION: n is a, c, g or t
165 <220> FEATURE:
166 <221> NAME/KEY: misc_feature /
167 <222> LOCATION: (15)..(15) /
168 <223> OTHER INFORMATION: n is a, c, g, or t
170 <400> SEQUENCE: 8
W--> 171 ttngargayc ayytngargg          20
174 <210> SEQ ID NO: 9
175 <211> LENGTH: 20
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial
179 <220> FEATURE:
180 <223> OTHER INFORMATION: antisense primer
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: (18)..(18) /
186 <223> OTHER INFORMATION: n is a, c, g, or t
188 <400> SEQUENCE: 9
W--> 189 ttrtgdatrt cdatrtgngc          20
192 <210> SEQ ID NO: 10
193 <211> LENGTH: 23
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial
197 <220> FEATURE:
198 <223> OTHER INFORMATION: forward primer
200 <400> SEQUENCE: 10
201 ggtggcacga ctcctggagc ccg          23
204 <210> SEQ ID NO: 11
205 <211> LENGTH: 24
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial
209 <220> FEATURE:
210 <223> OTHER INFORMATION: reverse primer
212 <400> SEQUENCE: 11
213 ttgacaccag accaactggt aatg          24
216 <210> SEQ ID NO: 12
217 <211> LENGTH: 440

```

RAW SEQUENCE LISTING

DATE: 12/07/2006

PATENT APPLICATION: US/09/910,208C

TIME: 08:54:18

Input Set : F:\MM4454.ST25.txt

Output Set: N:\CRF4\12072006\I910208C.raw

218 <212> TYPE: DNA *OK because source is listed*
 219 <213> ORGANISM: human calcium-binding protein
 222 <220> FEATURE:
 223 <221> NAME/KEY: exon
 224 <222> LOCATION: (22)..(297)
 225 <223> OTHER INFORMATION: Deduced amino acid sequence for human calcium-binding protein

227 <400> SEQUENCE: 12

228	ggttaacatt aggctgggaa g atg aca aaa ctt gaa gag cat ctg gag gga	51
229	Met Thr Lys Leu Glu Glu His Leu Glu Gly	
230	1 5 10	
232	att gtc aat atc ttc cac caa tac tca gtt cgg aag ggg cat ttt gac	99
233	Ile Val Asn Ile Phe His Gln Tyr Ser Val Arg Lys Gly His Phe Asp	
234	15 20 25	
236	acc ctc tct aag ggt gag ctg aag cag ctg ctt aca aag gag ctt gca	147
237	Thr Leu Ser Lys Gly Glu Leu Lys Gln Leu Leu Thr Lys Glu Leu Ala	
238	30 35 40	
240	aac acc atc aag aat atc aaa gat aaa gct gtc att gat gaa ata ttc	195
241	Asn Thr Ile Lys Asn Ile Lys Asp Lys Ala Val Ile Asp Glu Ile Phe	
242	45 50 55	
244	caa ggc ctg gat gct aat caa gat gaa cag gtc gac ttt caa gaa ttc	243
245	Gln Gly Leu Asp Ala Asn Gln Asp Glu Gln Val Asp Phe Gln Glu Phe	
246	60 65 70	
248	ata tcc ctg gta gcc att gcg ctg aag gct gcc cat tac cac acc cac	291
249	Ile Ser Leu Val Ala Ile Ala Leu Lys Ala Ala His Tyr His Thr His	
250	75 80 85 90	
252	aaa gag taggtagctc tctgaagctt tttacccagc aatgtcctca atgaggggtct	347
253	Lys Glu	
256	tttcttttccc tcaccaaaaac ccagccttgc ccgtggggag taagagttaa taaacacact	407
258	cacgaaaagt taaaaaaaaa aaaaaaaaaat tct	440
261	<210> SEQ ID NO: 13	
262	<211> LENGTH: 20	
263	<212> TYPE: DNA	
264	<213> ORGANISM: Artificial	
266	<220> FEATURE:	
267	<223> OTHER INFORMATION: sense primer	
269	<400> SEQUENCE: 13	
270	actatcaaca tcttccacca	20
273	<210> SEQ ID NO: 14	
274	<211> LENGTH: 20	
275	<212> TYPE: DNA	
276	<213> ORGANISM: artificial	
278	<220> FEATURE:	
279	<223> OTHER INFORMATION: antisense primer	
281	<400> SEQUENCE: 14	
282	tctttatcgg catccaggtc	20
285	<210> SEQ ID NO: 15	
286	<211> LENGTH: 15	
287	<212> TYPE: DNA	
288	<213> ORGANISM: Artificial	

RAW SEQUENCE LISTING

DATE: 12/07/2006

PATENT APPLICATION: US/09/910,208C

TIME: 08:54:18

Input Set : F:\MM4454.ST25.txt

Output Set: N:\CRF4\12072006\I910208C.raw

290 <220> FEATURE:
 291 <223> OTHER INFORMATION: primer PMN.HP7S 1-15
 293 <400> SEQUENCE: 15
 294 tactcagttc ggaag 15
 297 <210> SEQ ID NO: 16
 298 <211> LENGTH: 15
 299 <212> TYPE: DNA
 300 <213> ORGANISM: Artificial
 302 <220> FEATURE:
 303 <223> OTHER INFORMATION: primer PMN.HP7A 126-112
 305 <400> SEQUENCE: 16
 306 ttggaatatt tcac 15
 309 <210> SEQ ID NO: 17
 310 <211> LENGTH: 20
 311 <212> TYPE: DNA
 312 <213> ORGANISM: Artificial
 314 <220> FEATURE:
 315 <223> OTHER INFORMATION: primer HP7S 7-26
 317 <400> SEQUENCE: 17
 318 acattaggct gggaagatga 20
 321 <210> SEQ ID NO: 18
 322 <211> LENGTH: 20
 323 <212> TYPE: DNA
 324 <213> ORGANISM: Artificial
 326 <220> FEATURE:
 327 <223> OTHER INFORMATION: primer HP7A 336-317
 329 <400> SEQUENCE: 18
 330 ggacattgct gggtaaaaag 20
 333 <210> SEQ ID NO: 19
 334 <211> LENGTH: 92 *same even as page 1*
 335 <212> TYPE: PRT
 336 <213> ORGANISM: calcium binding protein
 339 <220> FEATURE:
 340 <221> NAME/KEY: misc_feature
 341 <222> LOCATION: (1)..(92)
 342 <223> OTHER INFORMATION: Amino acid sequence of SEQ ID No. 1
 344 <400> SEQUENCE: 19
 346 Met Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His
 347 1 5 10 15
 350 Glu Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu
 351 20 25 30
 354 Leu Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr
 355 35 40 45
 358 Lys Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp
 359 50 55 60
 362 Lys Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg
 363 65 70 75 80
 366 Val Leu Lys Thr Ala His Ile Asp Ile His Lys Glu
 367 85 90

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/910,208C

DATE: 12/07/2006
TIME: 08:54:19

Input Set : F:\MM4454.ST25.txt
Output Set: N:\CRF4\12072006\I910208C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 3,15
Seq#:9; N Pos. 18

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,13,14,15,16,17,18

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/910,208C

DATE: 12/07/2006

TIME: 08:54:19

Input Set : F:\MM4454.ST25.txt

Output Set: N:\CRF4\12072006\I910208C.raw

L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0

L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0

Notice to Comply	Application No.	Applicant(s)	
	09/910,208	HITOMI ET AL.	
	Examiner	Art Unit	
	Maher M. Haddad	1644	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
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